REMARKS

It is believed that by submitting the present amendment and sequence listing diskette, the application now fully complies with the requirements of 37 CFR 1.821-1.825. Favorable action by the examiner is solicited.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11-0345. Please credit any excess fees to such deposit account.

Respectfully submitted,

KEIL & WEINKAUF

Herbert B. Keil
Reg. No. 18,967

1350 Connecticut Ave., N.W.
Washington, D.C. 20036
(202)659-0100

HBK/DSK/kas

VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION

Delete the previously submitted sequence listing and substitute with the sequence listing shown on attached replacement pages 1-4.

Amend the paragraph on page 5, lines 15-20 as follows:

The variables X^1 to X^6 in the sequence His-X^1-His-X^2-X^3-X^4-Cys-X^5-X^6-Cys, (SEQ ID NO:1) may have the various preferred meanings independently of one another, with individual variables up to a maximum of five of the variables being an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His.

Amend the paragraph on page 13, line 5, as follows:

His-X^1-His-X^2-X^3-X^4-Cys-X^5-X^6-Cys (SEQ ID NO:1),

IN THE CLAIMS

Amend claims 1, 6 and 15 as follows:

1. (amended) A peptide fragment having the general sequence

His-X^1-His-X^2-X^3-X^4-Cys-X^5-X^6-Cys, (SEQ ID NO:1)

where the variables X^1 to X^6 in the sequence have the following meanings:

X^1 = an amino acid selected from the group of Ala, Val, Phe, Ser, Met, Trp, Tyr, Asn, Asp or Lys and the variables X^2 to X^6 an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^2 = an amino acid selected from the group of Val, Ile, Phe, Pro, Trp, Tyr, Gln, Glu or Arg and the variables X^1, X^3 to X^6 an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^3 = an amino acid selected from the group of Gly, Ile, Thr, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His and the variables X^1, X^2, X^4 to X^6 an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^4 = an amino acid selected from the group of Val, Phe, Pro, Cys, Met, Trp, Asn, Glu, Arg or His and the variables X^1 to X^3, X^5, X^6 an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^5 = an amino acid selected from the group of Gly, Ser, Cys, Met, Trp, Asn, Glu, Lys or Arg and the variables X^1 to X^4, X^6 an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^6 = an amino acid selected from the group of Phe, Pro, Ser, Cys, Trp, Tyr or Gln and the variables X^1 to X^5 an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His and

where at least one of the variables X^1 to X^6 in the sequence is, independently of one another, Gln or Asn.

6. (amended) A peptide fragment having the sequence

His-Gln-His-Glu-Gly-Arg-Cys-Lys-Glu-Cys (SEQ ID NO:2)

His-Asn-His-Arg-Tyr-Gly-Cys-Gly-Cys-Cys (SEQ ID NO:3)

His-Arg-His-Gly-Thr-Asn-Cys-Leu-Lys-Cys (SEQ ID NO:4)

His-Ile-His-Gln-Ser-Asn-Cys-Gln-Val-Cys (SEQ ID NO:5).

15. (amended) A process for preparing protein fragments able to enter into a reversible affinity linkage with immobilized metal ions, which comprises carrying out the following steps:

a) preparing a nucleic acid library starting from any suitable nucleic acid sequence which codes for a protein fragment of the sequence

His-X^1-His-X^2-X^3-X^4-Cys-X^5-X^6-Cys (SEQ ID NO:11),

where the histidine and cysteine residues of the sequence are conserved in the nucleic acid library,

b) fusing the nucleic acids of the library to a reporter gene which makes it possible to detect the fusion protein encoded by the resulting nucleic acid via its binding to the immobilized metal ions and

c) selecting the nucleic acid sequences which display a reversible binding to the immobilized metal ions which is at least 1.5 times stronger than the sequence in the natural Helicobacter pylori ATPase-439.